Methods & Materials: Acute febrile patients with no evident cause of fever attending a health centre in a suburban area of Maputo city in Mozambique between January and September 2013 were consecutively enrolled. Study area is characterized by poverty, poor sanitation, high prevalence of malaria and households are precarious. Main source of income is informal sector. Paired acute and convalescent samples were requested from each participant. Convalescent samples were initially screened for IgG anti-CHIKV using commercial indirect immunofluorescence test (IIFT) (EUROIMMUN AG, Lüebeck, Germany) and if positive, the corresponding acute sample was screened using the same test.

Results: Four hundred forty two patients were enrolled, but only 274 (61.9%) returned to the convalescent visit. The median age of study participants was 27.0 years and 59% (249/242) was female. Out of 46 (16.8%) convalescent samples were positive for IgG anti-CHIKV. The corresponding acute samples were also screened for IgG anti-CHKV and out of these, 5 were negative, suggesting a seroconversion rate of 2.0%. Four-fold titre rise of IgG anti-CHIKV was confirmed for 7 samples. Most of the positive samples clustered around August and September.

Conclusion: This report represents the first evidence of circulation of CHIKV in Mozambique. Seroconversion rate and titre rise of IgG anti-CHIKV strongly suggest that CHIKV is circulating in Mozambique, causing acute infection in suburban area of Maputo city. As a next step, all samples suggestive of acute infection by CHIKV will be screened using IIFT IgM anti-CHIKV in order to confirm acute infection and attempt to isolate the virus in cell culture is ongoing. We recommend that further studies should be conducted to investigate if CHIKV is causing sporadic cases, unsuspected outbreaks or if it has become an endemic virus.

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Using network analysis technique to describe the spread of Marburg hemorrhagic fever outbreak in Uganda, 2012

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Background: There was simultaneous outbreak of Marburg in Kabale, Ibanda and Kamwenge districts in Uganda in 2012 that started as a cluster of deaths due to a strange illness. The initial case investigation traced the transimission to a 33-year old male, a teacher at Nyakatukura Secondary School in Ibanda district. Between 19th October 2012 and 4th January 2013, 26 cases (15 confirmed and 5 probable), including 15 deaths (CFR of 75%), were registered in Kabale/ Kampala and Ibanda districts. A total of 327 contacts were listed from Kabale and Ibanda and followed up for the mandatory 21 days. We modelled the spread of the virus from index case using network analysis technique to determine the relationships and linkages between the affected individuals.

Methods & Materials: The study design was snowball network design whereby we started with first reported cases and asked them about their relations or contacts back in time, otherwise known as contact tracing. We defined our boundary as those patients that were infected by the Marburg virus. Our link relationship was contact between two individuals. Cases were entered into an adjacency matrix in Excel spreadsheet. The matrix was imported into network analysis software Visualizer®2.1 to construct the network and linkages. Degrees of centrality, betweenness, closeness and eigenvector were computed

Results: Two clusters of the outbreak were identified by Network analysis, one in Kabale district and another in Ibanda district. Twenty six (26) cases were linked to each other with thirty eight (38) linkages with degree centralization of 96.3%, closeness centrality of 29.2% and betweenness centralization of 58.3%. Close contact was responsible for the transmission and death occurred when the relationships was close such as husband and wife or child and mother. We identified an amplifier status as some of the patients were liked to many cases and death while they themselves did not die.

Conclusion: Close contact is key for the Spread of Marburg virus and usually result in death. Two clusters with an amplifier status were identified. High degree of centrality and betweenness indicate increase transmission between the cases. Increased surveillance is needed to reduce the spread of virus.

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Molecular evolution of Zika virus during its emergence in the 20th century

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Background: Zika virus (ZIKV) is mosquito-borne flavivirus first isolated in Uganda in 1947and repeatedly isolated by entomological and virological surveillance in sub-Saharan Africa and South East Asia. Until 2000, only few human cases were reported but in 2007, the first major human outbreak was notified in Yap Island, Micronesia leading to 99 cases. More recently in October 2013, more than 400 of ZIKV infections were reported in French Polynesia.